Amendments to the Specification

Please replace the section BRIEF DESCRIPTION OF THE DRAWINGS with the replacement section below (amendments underlined):

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows MALDI mass spectra of SEQ ID NO: 1, Angiotensin II (DRVYIHPF) (A) 157 nm photodissociation with DHB matrix (B) Post-source decay using CHCA matrix (C) AP MALDI collision induced dissociation. Fragments labeled with * involve loss of NH_3.

FIG. 2 shows MALDI mass spectra of SEQ ID NO: 2, a Hemoglobin tryptic peptide (LLVVYPWTQR) (A) 157 nm photodissociation using DHB as matrix (B) Post-source decay using CHCA matrix. (C) AP MALDI collision-induced dissociation. Peaks labeled I represent internal fragmentation.

FIG. 3 shows MALDI mass spectra of SEQ ID NO: 3, the peptide FSWGAEGQR (A) 157 nm photodissociation using DHB as matrix (B) Post-source decay using CHCA matrix. (C) AP MALDI collision-induced dissociation, (D) 2-keV TOF-TOF collision-induced dissociation. The * and ** labels represent the loss of one and two NH_3 groups, respectively.

FIG. 4 shows four typical mass spectra of peptides with basic residues (arginine) at their C-termini that were fragmented using 157-nm photodissociation. Each spectrum is dominated by *x*, *v*, and *w* fragments. The *w* fragments were observed at leucine residues, rendering them distinguishable from isoleucine. It is believed that the *b*- and *y*-type ions appearing in these spectra generally correspond to intense PSD fragments that were not completely eliminated with background subtraction. A) SEQ ID NO: 4, ALELFR; B) SEQ ID NO: 5, LFEELAR; C) SEQ ID NO: 6, IENHEGVR; D) SEQ ID NO: 7, EGVNDNEEGFFSAR. Peaks labeled Int are internal fragments. The * label represents the loss of one NH3 group.

FIG. 5 shows an illustrative apparatus 10 for analyzing high molecular weight compounds by fragmentation.

FIG. 6 shows an illustrative apparatus 50 for analyzing high molecular weight compounds by fragmentation.

Please replace the paragraph starting page 14, line 32 of the specification with the following paragraph (amendments underlined):

EXAMPLE 1. MALDI mass spectra of SEQ ID NO: 1, Angiotensin II (DRVYIHPF).

Please replace the paragraph starting page 15, line 14 of the specification with the following paragraph (amendments underlined):

EXAMPLE 2. MALDI mass spectra of SEQ ID NO: 2, a Hemoglobin tryptic peptide (LLVVYPWTQR).

Please replace the paragraph starting page 16, line 8 of the specification with the following paragraph (amendments underlined):

EXAMPLE 3. MALDI mass spectra of SEQ ID NO: 3, the peptide FSWGAEGQR.

Please replace the paragraph starting page 16, line 9 of the specification with the following paragraph (amendments underlined):

The mass spectrum of the photoproducts from the 157 nm dissociation of singly-charged SEQ ID NO: 3, FSWGAEGQR ions is shown in FIG. 3A. In contrast to Angiotensin II, this spectrum was dominated by *x* and *v* ions. The *x* ions correspond to cleavage of the same α-carbon--carbonyl carbon backbone bond that breaks to form an *a* ion except that the charge remained on the C-terminal fragment. The *v* ions are high-energy C-terminal fragments that are believed to originate from cleavage of the α-carbon--carbonyl carbon backbone bond followed by loss of CO and an amino acid side chain. It is believed that the concomitant appearance of both *x* and *v* type ions suggests that 157 nm photodissociation of peptides involves a radical cleavage process. Since the mass difference between x_n and v_{n+1} is constant, these ion pairs in the spectrum were readily identified. In addition to the *x* and *v* ions, peaks corresponding to the neutral loss of the side chains of glutamine, glutamic acid, and tryptophan from the intact precursor also appeared between 900 and 1000 daltons, as shown in FIG. 3A. Neutral losses have also been reported with ECD, where protonated side chains are specifically fragmented. *See*, H. J. Cooper, R. R. Hudgins, K. Håkansson, A. G. Marshall, *J. Am. Soc. Mass Spectrom.* **13,** 241 (2001). The post-source decay spectrum of the peptide SEQ ID NO: 3, FSWGAEGQR (FIG. 3B) contained nearly only the *y* and *b* ion series, as well as a large number of $y\text{-}NH_3$ fragments.

Considerable peak intensity variation was again observed. Many peaks corresponding to internal fragments (left unlabeled for clarity), in which the backbone was cleaved twice, were also observed from this peptide. The CID spectrum obtained by atmospheric pressure MALDI, shown in FIG. 3C, is similar to that obtained by PSD.

Please replace the paragraph starting page 16, line 30 of the specification with the following paragraph (amendments underlined):

EXAMPLE 4. MALDI mass spectra of the peptides SEQ ID NO: 4, ALELFR, SEQ ID NO: 5, LFEELAR, SEQ ID NO: 6, IENHEGVR, and SEQ ID NO: 7, EGVNDNEEGFFSAR.

Please replace the paragraph starting page 16, line 32 of the specification with the following paragraph (amendments underlined):

The mass spectrum of the photoproducts from the 157 nm dissociation of singly-charged SEQ ID NO: 4, ALELFR, SEQ ID NO: 5, LFEELAR, SEQ ID NO: 6, IENHEGVR, and SEQ ID NO: 7, EGVNDNEEGFFSAR ions are shown in FIG. 4. These spectra were generated following the general procedure described in Example 1, where A) is SEQ ID NO: 4, ALELFR, B) is SEQ ID NO: 5, LFEELAR, C) is SEQ ID NO: 6, IENHEGVR, and D) is SEQ ID NO: 7, EGVNDNEEGFFSAR.